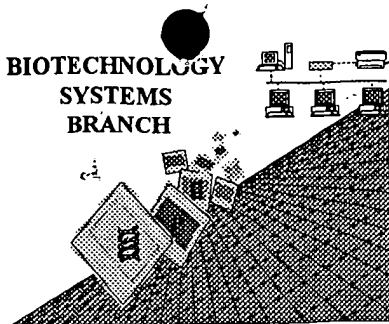


S. Rawlings

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/068,377B
Source: 1600
Date Processed by STIC: 2/20/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/068377B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1. Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
 Wrapped Aminos was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
 prevent "wrapping."

2. Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3. Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
 Numbering use space characters, instead.

4. Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
 ensure your subsequent submission is saved in ASCII text.

5. Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules,
 each n or Xaa can only represent a single residue. Please present the maximum number of each
 residue having variable length and indicate in the <220>-<223> section that some may be missing.

6. PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
 "bug" sequences(s) . Normally, PatentIn would automatically generate this section from the
 previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
 the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
 Artificial or Unknown sequences.

7. Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8. Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 (NEW RULES) <210> sequence id number
 <400> sequence id number
 000

9. Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
 (NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10. Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
 Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
 is Artificial Sequence

11. Use of <220> Sequence(s) 27 missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
 "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12. PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
 "bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
 listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

1642

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/068,377B

DATE: 07/20/2001

TIME: 13:33:24

Input Set : A:\GENENT061CP2seqlist.txt

Output Set: N:\CRF3\07202001\I068377B.raw

*Does Not Comply
Corrected Diskette Needed*

3 <110> APPLICANT: Lasky, Laurence A.
4 Dowbenko, Donald J.
6 <120> TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage Furrow-Associated
7 Proteins (PSTPIPs)
9 <130> FILE REFERENCE: P1066P2
11 <140> CURRENT APPLICATION NUMBER: US 09/068,377B
12 <141> CURRENT FILING DATE: 1998-05-08
14 <150> PRIOR APPLICATION NUMBER: PCT/US98/01774
15 <151> PRIOR FILING DATE: 1998-01-30
17 <150> PRIOR APPLICATION NUMBER: US 08/938,830
18 <151> PRIOR FILING DATE: 1997-09-29
20 <150> PRIOR APPLICATION NUMBER: US 60/104,589
21 <151> PRIOR FILING DATE: 1997-02-07
23 <160> NUMBER OF SEQ ID NOS: 73

ERRORED SEQUENCES

1343 <210> SEQ ID NO: 73
1344 <211> LENGTH: 34
1345 <212> TYPE: DNA
1346 <213> ORGANISM: Artificial Sequence
1348 <220> FEATURE:
1349 <223> OTHER INFORMATION: Synthetic oligonucleotide probe
1351 <400> SEQUENCE: 73
1352 attacacccg tgcgcctct gcaggaggat cccg 34

E--> 1354 1
E--> 1357 2
E--> 1360 1

delete

see next page for more error

09/068,377B

2

<210> 27

<211> 4

<212> PRT

<213> Artificial Sequence

see item 11 on Eru summary sheet

<220>

<223> Any amino acid

<400> 27

Pro Xaa Xaa Pro

1

<221>
<222>

These mandatory numerical identifiers need to be under <220> and lead response whenever Xaa (or 'n') is shown.

See 1.823 of Sequence Rules

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/068,377B

DATE: 07/20/2001

TIME: 13:33:25

Input Set : A:\GENENT061CP2seqlist.txt

Output Set: N:\CRF3\07202001\I068377B.raw

L:708 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:27
L:708 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:708 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1354 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:34 SEQ:73
M:254 Repeated in SeqNo=73